

SEQUENCE LISTING

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<120> NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS
AND THERAPY OF PROSTATE AND COLON CANCER

<130> 129.9USI1

<150> 09/323,597

<151> 1999-06-01

<160> 29

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<210> 1

<211> 1738

<212> DNA

<213> Homo Sapiens

<220>

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                                     Met Ala
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ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac cat      165
Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His
      5                      10                      15

gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc      213
Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro
      20                      25                      30

act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc      261
Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro
      35                      40                      45                      50

cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc tgc      309
Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys
      55                      60                      65

acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act aag      357
Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys
      70                      75                      80

aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct      405
Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala

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95

aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct 501
Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser
115 120 125 130

aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag aat 549
Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn
135 140 145

cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca 597
 Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser
 150 155 160

tct cag agg aag tcc tgg cac cct gcg tgc caa gac gac tgg aac gag 645
Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu
165 170 175

aac tac ggg cgg gcg gcc tgc agg gac / atg ggc tat aag aat aat ttt 693
Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe
180 185 190

tac	tct	agc	caa	gga	ata	gtg	gat	gac	agc	gga	tcc	acc	agc	ttt	atg	741
Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser	Phe	Met	
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aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg tac 789
Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr
215 220 225

cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata 837
His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile
230 235 240

gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc 885
Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly
245 250 255

ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac 933
Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His
260 265 270

gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag tgg 981
Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp
275 280 285 290

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Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn	Pro	Trp	
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cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat 1077
His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr
310 315 320

gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat ~~tat~~ gac 1125
Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn ~~Tyr~~ Asp
325 330 335

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2

072000

Debut

SECRET

3

002720 58257960

Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
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 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
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 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
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 225 230 235 240
 Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
 245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
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 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
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 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
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 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
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 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
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 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
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59

Ref C1

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cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc	155
His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val	
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Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val	
35 40 45	
ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc	251
Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val	
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tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act	299
Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr	
70 75 80	
aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga	347
Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly	
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Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu	
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Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met Tyr	
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Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn	
180 185 190	
ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt	683
Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe	
195 200 205	
atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg	731
Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu	
210 215 220 225	
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Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys	
230 235 240	
tta gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg atc gtg	827
Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val	
245 250 255	

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 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
 245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
 325 330 335

EWCT

Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
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Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
355 360 365
Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
370 375 380
Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
385 390 395 400
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Sub C7

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Sub C1

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